

SUS
#16

FIGURE 1A

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | AAG | CCG | TAC | TTC | TGC | CGT | GTC | TTT | GTC | TTC | TGC | TTC | CTA | ATC | 45 |
| M | K | P | Y | F | C | R | V | F | V | F | C | F | L | I | |
| | | | | 5 | | | | | 10 | | | | | 15 | |
| AGA | CTT | TTA | ACA | GGA | GAA | ATC | AAT | GGC | TCG | GCC | GAT | CAT | AGG | ATG | 90 |
| R | A | L | T | G | E | I | N | G | S | A | D | H | R | M | |
| | | | | 20 | | | | | 25 | | | | | 30 | |
| TTT | TCA | TTT | CAC | AAT | GGA | GGT | GTA | CAG | ATT | TCT | TGT | AAA | TAC | CCT | 135 |
| F | S | F | H | N | G | G | V | Q | I | S | C | K | Y | P | |
| | | | | 35 | | | | | 40 | | | | | 45 | |
| GAG | ACT | GTC | CAG | CAG | TTA | AAA | ATG | CGA | TTG | TTC | AGA | GAG | AGA | GAA | 180 |
| E | T | V | Q | Q | L | K | M | R | L | F | R | E | R | E | |
| | | | | 50 | | | | | 55 | | | | | 60 | |
| GTC | CTC | TGC | GAA | CTC | ACC | AAG | ACC | AAG | GGA | AGC | GGA | AAT | GCG | GTG | 225 |
| V | L | C | E | L | T | K | T | K | G | S | G | N | A | V | |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| TCC | ATC | AAG | AAT | CCA | ATG | CTC | TGT | CTA | TAT | CAT | CTG | TCA | AAC | AAC | 270 |
| S | I | K | N | P | M | L | C | L | Y | H | L | S | N | N | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| AGC | GTC | TCT | TTT | TTC | CTA | AAC | AAC | CCA | GAC | AGC | TCC | CAG | GGA | AGC | 315 |
| S | V | S | F | F | L | N | N | P | D | S | S | Q | G | S | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| TAT | TAC | TTC | TGC | AGC | CTG | TCC | ATT | TTT | GAC | CCA | CCT | CCT | TTT | CAA | 360 |
| Y | Y | F | C | S | L | S | I | F | D | P | P | P | F | Q | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| GAA | AGG | AAC | CTT | AGT | GGA | GGA | TAT | TTG | CAT | ATT | TAT | GAA | TCC | CAG | 405 |
| E | R | N | L | S | G | G | Y | L | H | I | Y | E | S | Q | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| CTC | TGC | TGC | CAG | CTG | AAG | CTC | TGG | CTA | CCC | GTA | GGG | TGT | GCA | GCT | 450 |
| L | C | C | Q | L | K | L | W | L | P | V | G | C | A | A | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| TTC | GTT | GTG | GTA | CTC | CTT | TTT | GGA | TGC | ATA | CTT | ATC | ATC | TGG | TTT | 495 |
| F | V | V | V | L | L | F | G | C | I | L | I | I | W | F | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| TCA | AAA | AAG | AAA | TAC | GGA | TCC | AGT | GTG | CAT | GAC | CCT | AAT | AGT | GAA | 540 |
| S | K | K | K | Y | G | S | S | V | H | D | P | N | S | E | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| TAC | ATG | TTC | ATG | GCG | GCA | GTC | AAC | ACA | AAC | AAA | AAG | TCT | AGA | CTT | 585 |
| Y | M | F | M | A | A | V | N | T | N | K | K | S | R | L | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| GCA | GGT | GTG | ACC | TCA | | | | | | | | | | | 600 |
| A | G | V | T | S | | | | | | | | | | | |
| | | | | 200 | | | | | | | | | | | |

003211 02432450

FIGURE 1B

| | | | | | | |
|-----------|------------|------------|------------|-------------|-------------|-----|
| mCRP1 | MKPYFCRVFV | FCFLIRLL-- | -----TGEIN | GS-----ADHR | MFSFHNGGVQ | 39 |
| mCD28 | MT----- | ----LRLLFL | ALNFFSVQVT | ENKILVKQSP | LLVVDSEVS | 38 |
| Consensus | M..... |RLL.. | | |V. | |
| mCRP1 | ISCKYPETV- | -QQLKMRLFR | --EREV-LCE | LTKTKGSGNA | VSIGNPMLCL | 34 |
| mCD28 | LSCRYSYNLL | AKEFRASLYK | GVNSDVEVCV | GNGNFTYQPQ | FRSNAEFNCD | 33 |
| Consensus | .SC.Y..... |L.. |V..C. | |C. | |
| mCRP1 | YHLSNNSVSF | FLNNPDSSQG | SYFCSLSIF | DPPPFQERNL | SGGYL-HIYE | 133 |
| mCD28 | GDFDNETVTF | RLWNLHVNHT | DIYFCKIEFM | YPPPYLDNER | SNGTIIHIKE | 133 |
| Consensus |N..V.F | .L.N..... | ..YFC..... | .PPP..... | S.G...HI.E | |
| mCRP1 | SQLC---CQL | KL-W-LPVGC | AA-FVVLLF | GCIL-IIWFS | KKKY-----GS | 172 |
| mCD28 | KHLCHTQSSP | KLFWALVVVA | GVLFYGLLV | TVALCVIWTN | SRNRLLQVT | 138 |
| Consensus | ..LC..... | KL.W.L.V.. | ...F...LL. | ...L..IW.. | | |
| mCRP1 | SVH-DPNSY | MFMAAVNTNK | KSR-LAGVTS | | | 200 |
| mCD28 | TMNMTPRRPG | LTRKPYQPYA | PARDFAAYRP | | | 218 |
| Consensus |P.... | | ..R..A.... | ... | | |

008277 0248260

FIGURE 2A

| | |
|---|-----|
| ATG CAG CTA AAG TGT CCC TGT TTT GTG TCC TTG GGA ACC AGG CAG | 45 |
| M Q L K C P C F V S E G T R Q | |
| 5 10 15 | |
| CCT GTT TGG AAG AAG CTC CAT GTT TCT AGC GGG TTC TTT TCT GGT | 90 |
| P V W K K L H V S S G F F S G | |
| 20 25 30 | |
| CTT GGT CTG TTC TTG CTG CTG TTG AGC AGC CTC TGT GCT GCC TCT | 135 |
| L G L F L L L L S S L C A A S | |
| 35 40 45 | |
| GCA GAG ACT GAA GTC GGT GCA ATG GTG GGC AGC AAT GTG GTG CTC | 180 |
| A E T E V G A M V G S N V V L | |
| 50 55 60 | |
| AGC TGC ATT GAC CCC CAC AGA CGC CAT TTC AAC TTG AGT GGT CTG | 225 |
| S C I D P H R R H F N L S G L | |
| 65 70 75 | |
| TAT GTC TAT TGG CAA ATC GAA AAC CCA GAA GTT TCG GTG ACT TAC | 270 |
| Y V Y W Q I E N P E V S V T Y | |
| 80 85 90 | |
| TAC CTG CCT TAC AAG TCT CCA GGG ATC AAT GTG GAC AGT TCC TAC | 315 |
| Y L P Y K S P G I N V D S S Y | |
| 95 100 105 | |
| AAG AAC AGG GGC CAT CTG TCC CTG GAC TCC ATG AAG CAG GGT AAC | 360 |
| K N R G H L S L D S M K Q G N | |
| 110 115 120 | |
| TTC TCT CTG TAC CTG AAG AAT GTC ACC CCT CAG GAT ACC CAG GAG | 405 |
| F S L Y L K N V T P Q D T Q E | |
| 125 130 135 | |
| TTC ACA TGC CGG GTA TTT ATG AAT ACA GCC ACA GAG TTA GTC AAG | 450 |
| F T C R V F M N T A T E L V K | |
| 140 145 150 | |
| ATC TTG GAA GAG GTG GTC AGG CTG CGT GTG GCA GCA AAC TTC AGT | 495 |
| I L E E V V R L R V A A N F S | |
| 155 160 165 | |
| ACA CCT GTC ATC AGC ACC TCT GAT AGC TCC AAC CCG GGC CAG GAA | 540 |
| T P V I S T S D S S N P G Q E | |
| 170 175 180 | |
| CGT ACC TAC ACC TGC ATG TCC AAG AAT GGC TAC CCA GAG CCC AAC | 585 |
| R T Y T C M S K N G Y P E P N | |
| 185 190 195 | |
| CTG TAT TGG ATC AAC ACA ACG GAC AAT AGC CTA ATA GAC ACG GCT | 630 |
| L Y W I N T T D N S L I D T A | |
| 200 205 210 | |
| CTG CAG AAT AAC ACT GTC TAC TTG AAC AAG TTG GGC CTG TAT GAT | 675 |
| L Q N N T V Y L N K L G L Y D | |
| 215 220 225 | |
| GTA ATC AGC ACA TTA AGG CTC CCT TGG ACA TCT CGT GGG GAT GTT | 720 |
| V I S T L R L P W T S R G D V | |
| 230 235 240 | |

003211 02482260

[illegible]

755
310
855
900
945
966

FIGURE 2B

| | | | | | | |
|-----------|------------|-------------|------------|-------------|------------|-----|
| mB7RP1 | MQLKPCFVS | LGTRQPVWKK | LHVSSGFFSG | LGLFLLLLS- | SLCAASAETE | 49 |
| mCD80 | MA--CNC--Q | LMQDTPL--- | LKFPCPRLI- | L-LFVLLIRL | SQVSSDVDEQ | 41 |
| Consensus | M...C.C... | L....P.... | L..... | L.LF.LL... | S..... | |
| mB7RP1 | VGAMVGSNVV | LSCIDPHRRH | FNLSGLYVYW | QIENPEVSVT | YYLPYKSPGI | 39 |
| mCD80 | LSKSVKDKVL | LPC-RYNsph | EDESEDRIYW | QKHDKVV--- | --LSVIAGKL | 35 |
| Consensus |V...V. | L.C.....H | ...S....YW | Q...V... | ..L..... | |
| mB7RP1 | NVDSSYKNRG | HLSLDSMKQG | NFSLYLKNVT | PQDTQEFTCR | VFMNTATELV | 149 |
| mCD80 | KVWPEYKNR- | --TL--YDNT | TYSLIILGLV | LSDRGTYSCV | VQKKERGTYE | 130 |
| Consensus | .V...YKNR. | ...L..... | ..SL..... | ..D.....C. | V..... | |
| mB7RP1 | KILEEVVRLR | VAANFSTPVI | STSDSSNPGQ | ERTYTCMSKN | GYPEPNLYWI | 199 |
| mCD80 | VKHLALVKLS | IKADFSTPNI | TESGNPSADT | KRI-TCFASG | GFPKPRFSWL | 179 |
| Consensus |V.L. | ...A.FSTP.I | ..S..... | .R..TC... | G.P.P...W. | |
| mB7RP1 | -NTTDSLID | TALQNTVYL | NKLGLYDVIS | TLRLPWTSRG | DVLCVENVA | 248 |
| mCD80 | ENGRELPGIN | TTISQDPESE | LYTISSQLDF | NTTRNHTIKC | LIKYGDAHVS | 229 |
| Consensus | .N.....I. | T..... | |T... |V. | |
| mB7RP1 | LHQNITSISQ | AESFTGNNTK | NPQETHNNEL | KVLVPVLAVL | A-AAAFVSFI | 297 |
| mCD80 | EDFTWEKPPE | DPPDSKNTLV | LFGAGFGAVI | TVVVIIVVIK | CFCKHRSCFR | 279 |
| Consensus | |N... | | .V.V.V..... |F. | |
| mB7RP1 | IYRRTR-PHR | SYT-GPKTVQ | LELTDHA | | | 322 |
| mCD80 | RNEASRETNM | SLTFGPPEAL | AEQTVFL | | | 306 |
| Consensus | ...R.... | S.T.GP... | .E.T... | | | |

003211 0242260

FIGURE 3A

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | CGG | CTG | GGC | AGT | CCT | GGA | CTG | CTC | TTC | CTG | CTC | TTC | AGC | AGC | 45 |
| M | R | L | G | S | P | G | L | L | F | L | L | F | S | S | |
| | | | | 5 | | | | | 10 | | | | | 15 | |
| CTT | CGA | GCT | GAT | ACT | CAG | GAG | AAG | GAA | GTC | AGA | GCG | ATG | GTA | GGC | 90 |
| L | R | A | D | T | Q | E | K | E | V | R | A | M | V | G | |
| | | | | 20 | | | | | 25 | | | | | 30 | |
| AGC | GAC | GTG | GAG | CTC | AGC | TGC | GCT | TGC | CCT | GAA | GGA | AGC | CGT | TTT | 135 |
| S | D | V | E | L | S | C | A | C | P | E | G | S | R | F | |
| | | | | 35 | | | | | 40 | | | | | 45 | |
| GAT | TTA | AAT | GAT | GTT | TAC | GTA | TAT | TGG | CAA | ACC | AGT | GAG | TCG | AAA | 180 |
| D | L | N | D | V | Y | V | Y | W | Q | T | S | E | S | K | |
| | | | | 50 | | | | | 55 | | | | | 60 | |
| ACC | GTG | GTG | ACC | TAC | CAC | ATC | CCA | CAG | AAC | AGC | TCC | TTG | GAA | AAC | 225 |
| T | V | V | T | Y | H | I | P | Q | N | S | S | L | E | N | |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| GTG | GAC | AGC | CGC | TAC | CGG | AAC | CGA | GCC | CTG | ATG | TCA | CCG | GCC | GGC | 270 |
| V | D | S | R | Y | R | N | R | A | L | M | S | P | A | G | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| ATG | CTG | CGG | GGC | GAC | TTC | TCC | CTG | CGC | TTG | TTC | AAC | GTC | ACC | CCC | 315 |
| M | L | R | G | D | F | S | L | R | L | F | N | V | T | P | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| CAG | GAC | GAG | CAG | AAG | TTT | CAC | TGC | CTG | GTG | TTG | AGC | CAA | TCC | CTG | 360 |
| Q | D | E | Q | K | F | H | C | L | V | L | S | Q | S | L | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| GGA | TTC | CAG | GAG | GTT | TTG | AGC | GTT | GAG | GTT | ACA | CTG | CAT | GTG | GCA | 405 |
| G | F | Q | E | V | L | S | V | E | V | T | L | H | V | A | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| GCA | AAC | TTC | AGC | GTG | CCC | GTC | GTC | AGC | GCC | CCC | CAC | AGC | CCC | TCC | 450 |
| A | N | F | S | V | P | V | V | S | A | P | H | S | P | S | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| CAG | GAT | GAG | CTC | ACC | TTC | ACG | TGT | ACA | TCC | ATA | AAC | GGC | TAC | CCC | 495 |
| Q | D | E | L | T | F | T | C | T | S | I | N | G | Y | P | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| AGG | CCC | AAC | GTG | TAC | TGG | ATC | AAT | AAG | ACG | GAC | AAC | AGC | CTG | CTG | 540 |
| R | P | N | V | Y | W | I | N | K | T | D | N | S | L | L | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| GAC | CAG | GCT | CTG | CAG | AAT | GAC | ACC | GTC | TTC | TTG | AAC | ATG | CGG | GGC | 585 |
| D | Q | A | L | Q | N | D | T | V | F | L | N | M | R | G | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| TTG | TAT | GAC | GTG | GTC | AGC | GTG | CTG | AGG | ATC | GCA | CGG | ACC | CCC | AGC | 630 |
| L | Y | D | V | V | S | V | L | R | I | A | R | T | P | S | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| GTG | AAC | ATT | GGC | TGC | TGC | ATA | GAG | AAC | GTG | CTT | CTG | CAG | CAG | AAC | 675 |
| V | N | I | G | C | C | I | E | N | V | L | L | Q | Q | N | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| CTG | ACT | GTC | GGC | AGC | CAG | ACA | GGA | AAT | GAC | ATC | GGA | GAG | AGA | GAC | 720 |
| L | T | V | G | S | Q | T | G | N | D | I | G | E | R | D | |
| | | | | 230 | | | | | 235 | | | | | 240 | |

09728420-112800

FIGURE 3A (Con't)

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAG | ATC | ACA | GAG | AAT | CCA | GTC | AGT | ACC | GGC | GAG | AAA | AAC | GCG | GCC | 765 |
| K | I | T | E | N | P | V | S | T | G | E | K | N | A | A | |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| ACG | TGG | AGC | ATC | CTG | GCT | GTC | CTG | TGC | CTG | CTT | GTG | GTC | GTG | GCG | 810 |
| T | W | S | I | L | A | V | L | C | L | L | V | V | V | A | |
| | | | | 250 | | | | | 265 | | | | | 270 | |
| GTG | GCC | ATA | GGC | TGG | GTG | TGC | AGG | GAC | CGA | TGC | CTC | CAA | CAC | AGC | 855 |
| V | A | I | G | W | V | C | R | D | R | C | L | Q | H | S | |
| | | | | 275 | | | | | 280 | | | | | 285 | |
| TAT | GCA | GGT | | | | | | | | | | | | | 864 |
| Y | A | G | | | | | | | | | | | | | |
| | | | | 288 | | | | | | | | | | | |

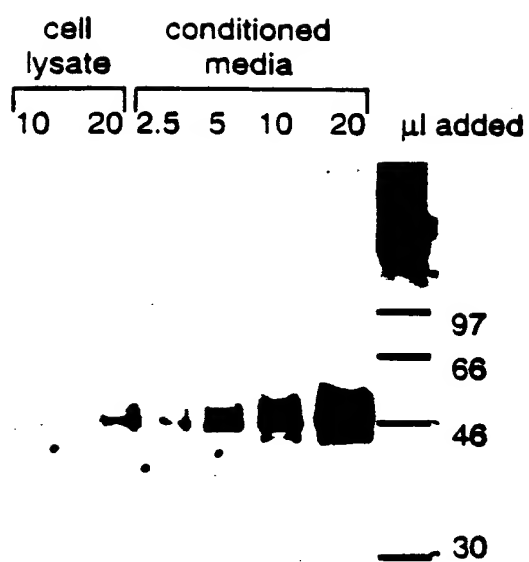
00821 02482260

FIGURE 3B

| | | | | | | |
|-----------|------------|------------|-------------|------------|--------------|-----|
| hB7RP1 | EKEVRAMVGS | DVELSCACPE | GSRFDLNDVY | VYWQTSESKT | VVTYHIPQNS | 50 |
| mB7RP1 | ETEVGAMVGS | NVVLSCIDPH | RRHFNLSGLY | VYWQIENPEV | SVTYLBYKS | 50 |
| Consensus | E.EV.AMVGS | .V.LSC..P. | ...F.L...Y | VYWQ..... | .VTY...P...S | |
| hB7RP1 | SLENVDSRYR | NRALMSPAGM | LRGDFSLRLF | NVTPQDEQKF | HCLVLSQ-SL | 99 |
| mB7RP1 | PGINVDSSYK | NRGHLSLDSM | KQGNFSLYLK | NVTPQDTQEF | TCRVFMTAT | 100 |
| Consensus | ...NVDS.Y. | NR...S...M | ..G.FSL.L. | NVTPQD.Q.F | .C.V..... | |
| hB7RP1 | GFQEVLSVEV | TLHVAANFSV | PVVSAPHSPS | Q-DELTFTCT | SINGYPRPNV | 143 |
| mB7RP1 | ELVKILEEVV | RLRVAANFST | PVISTSDSSN | PGQERTYTCM | SKNGYPEPNL | 150 |
| Consensus |L...V | .L.VAANFS. | PV.S...S... | ...E.T.TC. | S.NGYP.PN. | |
| hB7RP1 | YWINKTDNSL | LDQALQNDTV | FLNMRGLYDV | VSVLRIARTP | SVNIGCCIEH | 198 |
| mB7RP1 | YWINTTDNSL | IDTALQNNTV | YLNKLGLYDV | ISTLRLPWTS | RGDVLCCVEN | 200 |
| Consensus | YWIN.TDNSL | .D.ALQN.TV | .LN..GLYDV | .S.LR...T. |CC.EN | |
| hB7RP1 | VLLQQNLTVG | SQTGNDIGER | DKITENPVST | GEKNAATWSI | LAVLCLLVVV | 248 |
| mB7RP1 | VALHQNITSI | SQAESFTGNN | TKNPQETHNN | ELKVLV--PV | LAVLAAAFV | 248 |
| Consensus | V.L.QN.T.. | SQ...G... | .K....K... | ..K...7... | LAVL.....V | |
| hB7RP1 | AVAIGWVCRD | RCLQHSYAG | | | | 267 |
| mB7RP1 | SFIIYR--RT | R-PHRSYTGP | KTVQLELTDH | A | | 276 |
| Consensus | ...I...R. | R....SY.G. | | | | |

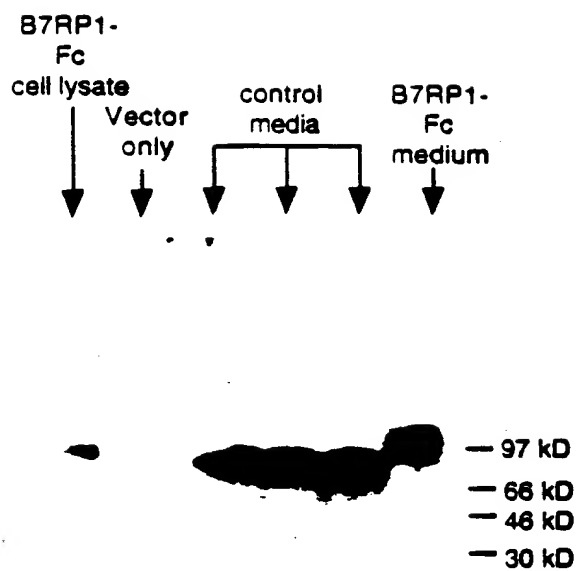
09728420 112800

Figure 4A



0928420-12800

Figure 4B



09723420 112800

Figure 5

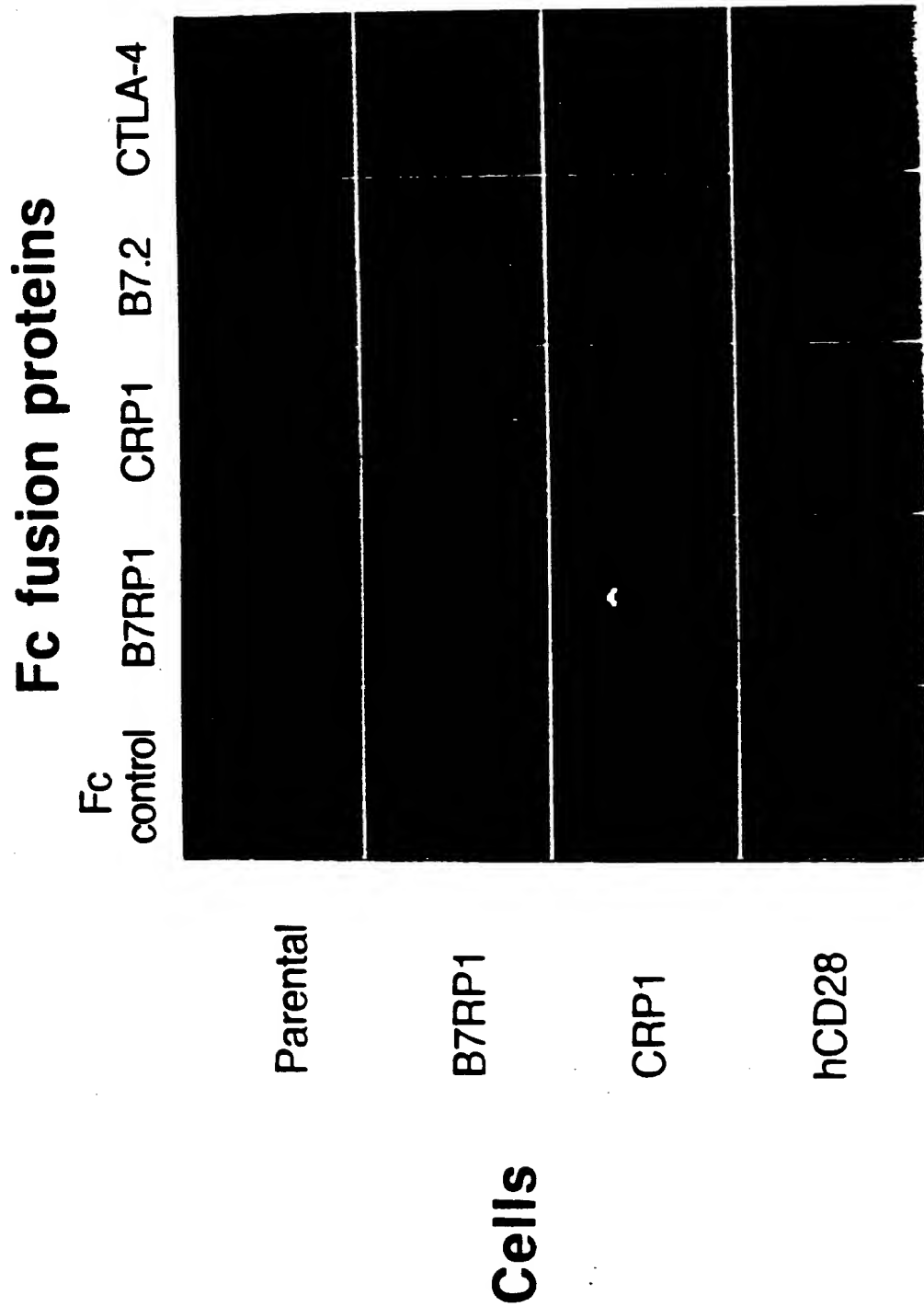


Figure 6

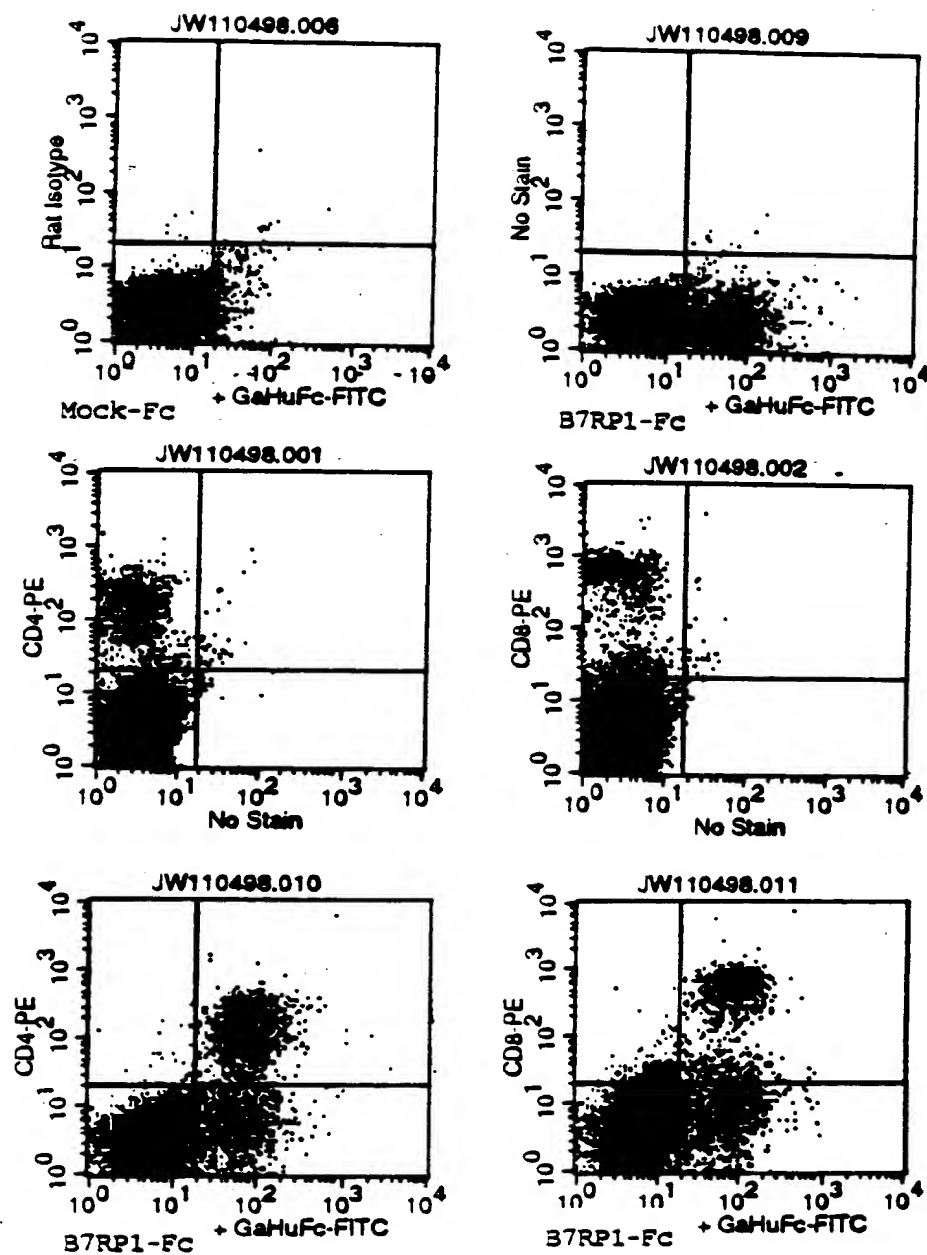
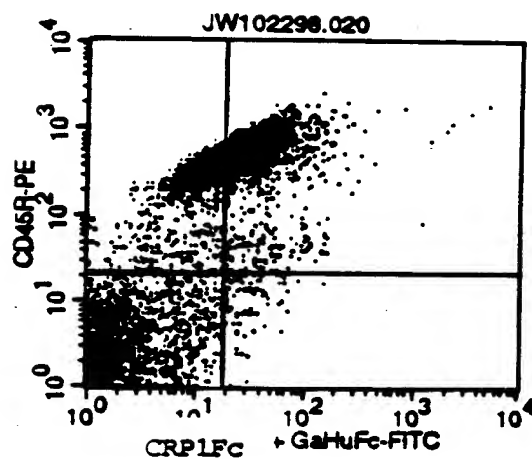
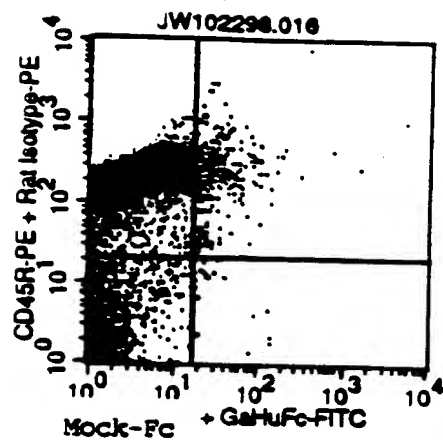
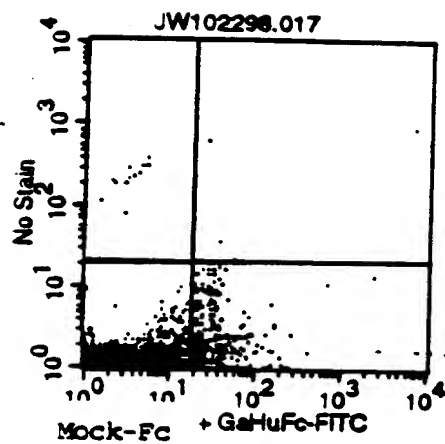
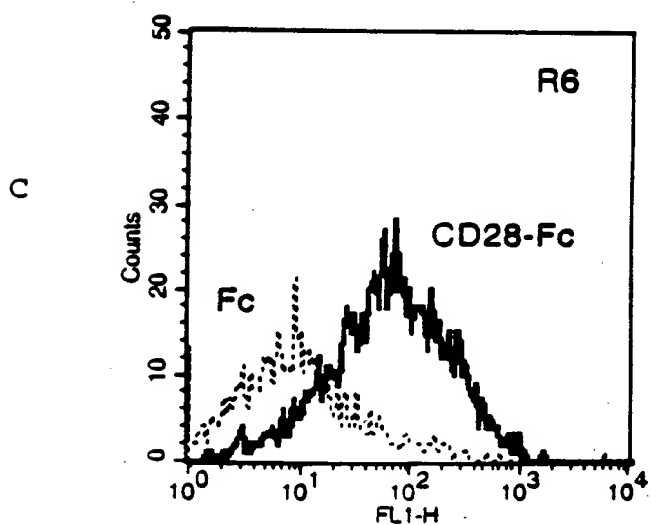
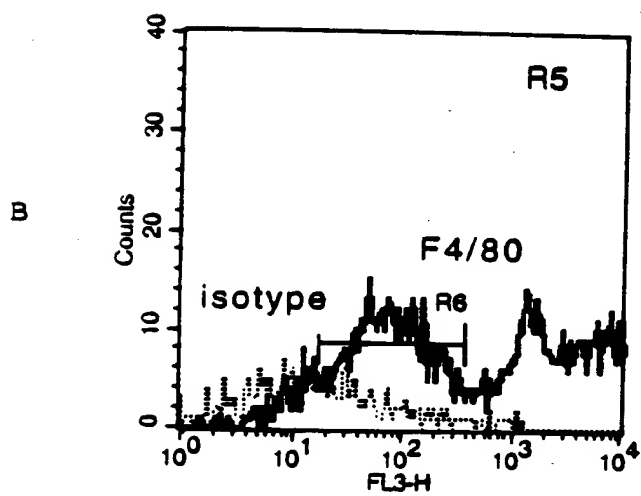
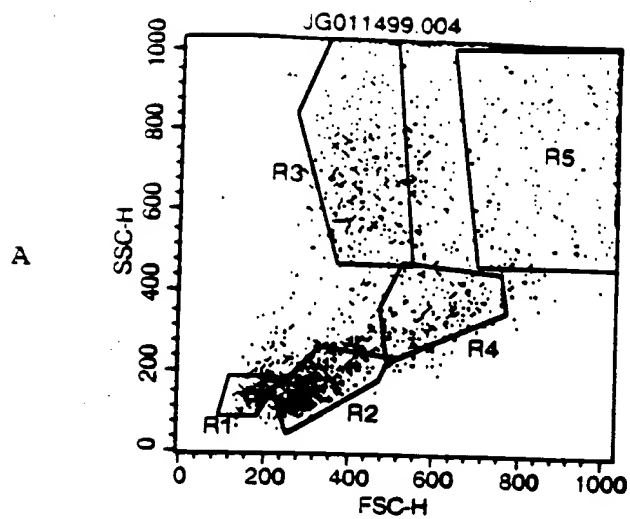


Figure 7



008211 02482460

Figure 3



008211 02482750

FIGURE 9

Con A stimulation of T-cells regulated
by B7RP1-Fc fusion protein

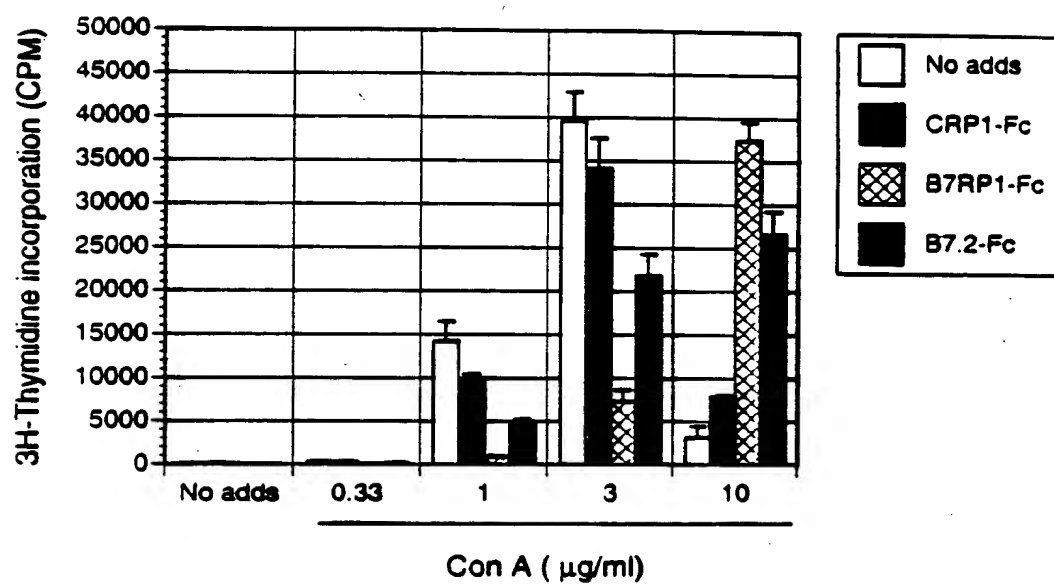


Figure 10

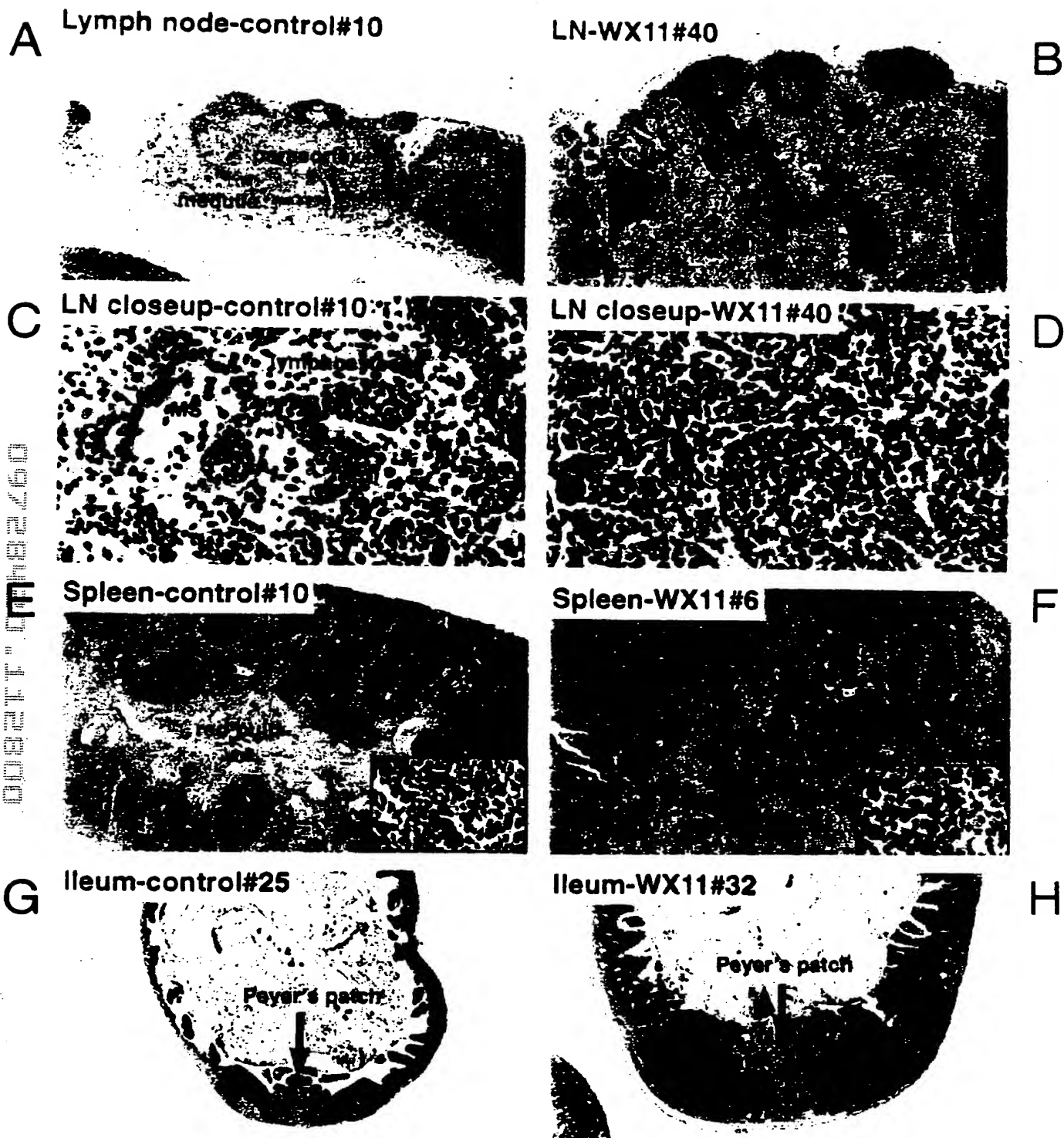


Figure 11

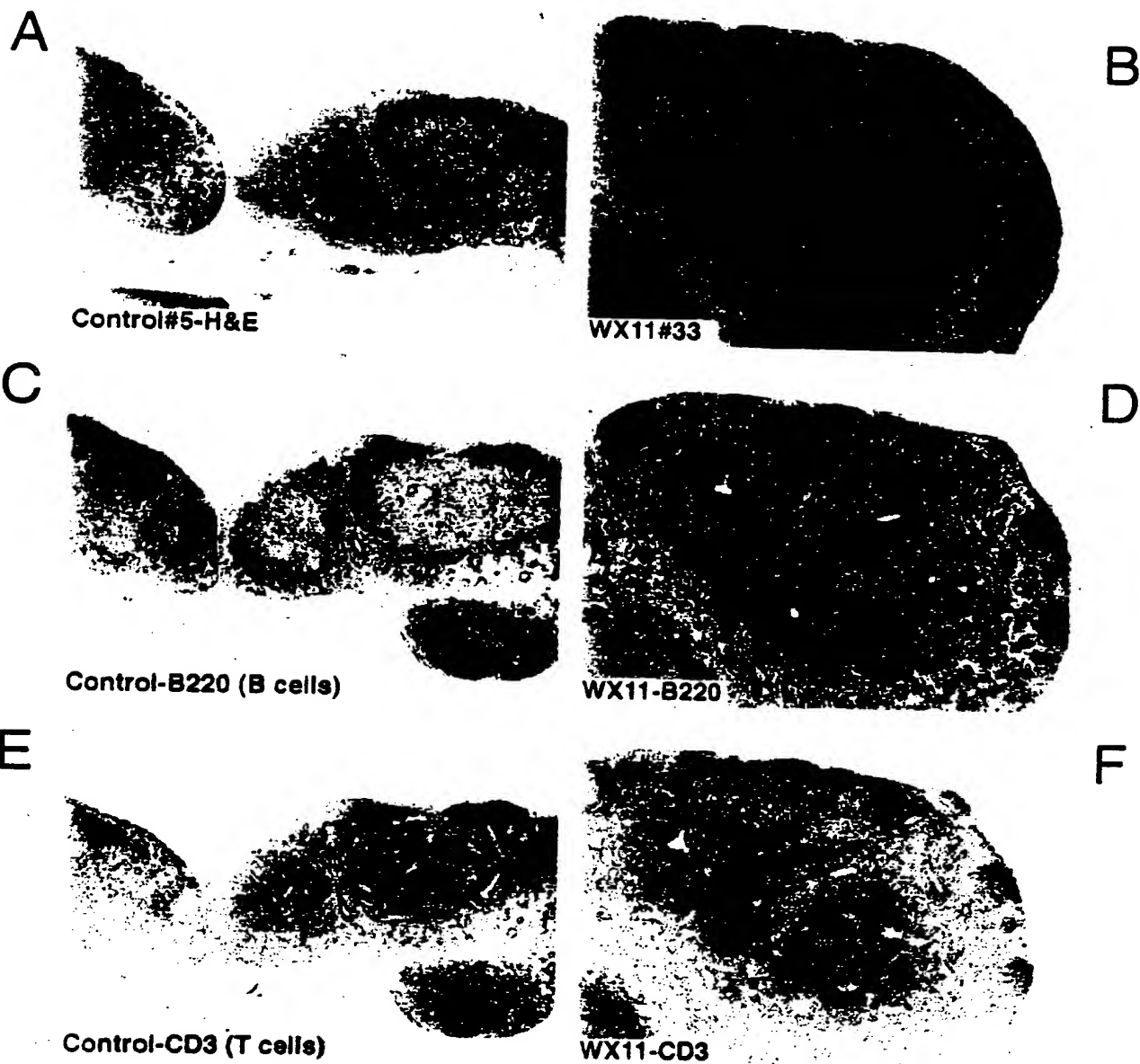


Figure 12A.

| | |
|---|------|
| GCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTTCGACCCACGCGTCCGCCCACGCG | -138 |
| TCCGCGGGAGCGCAGTTAGAGCCGATCTCCCGCGCCCCGAGGTTGCTCCTCTCCGAGGTCTC | -76 |
| CCGCGGCCCCAAGTTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGTCTCCGCGGCCCGAGGT | -14 |
| CTCCGCCCCGACC | -1 |
| ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC | 45 |
| M R L G S P G L L F L L F S S | |
| 5 10 15 | |
| CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC | 90 |
| L R A *D *T *Q *E K *E V R A *M V G | |
| 20 25 30 | |
| AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT | 135 |
| S D V E L S C A C P E G S R F | |
| 35 40 45 | |
| GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA | 180 |
| D L N D V Y V Y W Q T S E S K | |
| 50 55 60 | |
| ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC | 225 |
| T V V T Y H I P Q N S S L E N | |
| 65 70 75 | |
| GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC | 270 |
| V D S R Y R N R A L M S P A G | |
| 80 85 90 | |
| ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC | 315 |
| M L R G D F S L R L F N V T P | |
| 95 100 105 | |
| CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG | 360 |
| Q D E Q K F H C L V L S Q S L | |
| 110 115 120 | |
| GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA | 405 |
| G F Q E V L S V E V T L H V A | |
| 125 130 135 | |
| GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC | 450 |
| A N F S V P V V S A P H S P S | |
| 140 145 150 | |
| CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC | 495 |
| Q D E L T F T C T S I N G Y P | |
| 155 160 165 | |
| AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG | 540 |
| R P N V Y W I N K T D N S L L | |
| 170 175 180 | |
| GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC | 585 |
| D Q A L Q N D T V F L N M R G | |
| 185 190 195 | |
| TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC | 630 |
| L Y D V V S V L R I A R T P S | |
| 200 205 210 | |
| GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC | 675 |
| V N I G C C I E N V L L Q Q N | |
| 215 220 225 | |

00327 02482260

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| CTG | ACT | GTC | GGC | AGC | CAG | ACA | GGA | AAT | GAC | ATC | GGA | GAG | AGA | GAC | | 720 |
| L | T | V | G | S | Q | T | G | N | D | I | G | E | R | D | | |
| | | | | 230 | | | | | 235 | | | | | 240 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| AAG | ATC | ACA | GAG | AAT | CCA | GTC | AGT | ACC | GGC | GAG | AAA | AAC | GCG | GCC | | 765 |
| K | I | T | E | N | P | V | S | T | G | E | K | N | A | A | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| ACG | TGG | AGC | ATC | CTG | GCT | GTC | CTG | TGC | CTG | CTT | GTG | GTC | GTG | GCG | | 810 |
| T | W | S | L | L | A | V | L | C | L | L | V | V | V | A | | |
| | | | | 260 | | | | | 265 | | | | | 270 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| GTG | GCC | ATA | GGC | TGG | GTG | TGC | AGG | GAC | CGA | TGC | CTC | CAA | CAC | AGC | | 855 |
| V | A | I | G | W | V | C | R | D | R | C | L | Q | H | S | | |
| | | | | 275 | | | | | 280 | | | | | 285 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| TAT | GCA | GGT | GCC | TGG | GCT | GTG | AGT | CCG | GAG | ACA | GAG | CTC | ACT | GGC | | 900 |
| Y | A | G | A | W | A | V | S | P | E | T | E | L | T | G | | |
| | | | | | | | | | | | | | | 300 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|------|--|--|--|--|--|--|--|--|--|--|--|--|--|-----|
| CAC | GTT | TGA | | | | | | | | | | | | | | 909 |
| H | V | STOP | | | | | | | | | | | | | | |
| | | 302 | | | | | | | | | | | | | | |

| | | |
|--|--|------|
| CCGGAGCTCACC | CCCCAGAGCGTGGACAGGGCTTCCGTGAGACGCCACCGTGAGAGGCCAGG | 971 |
| TGGCAGCTTGAGCATGGACTCCCAGACTGCAGGGGAGCACTTGGGGCAGCCCCCAGAAGGAC | | 1033 |
| CACTGCTGGATCCCAGGGAGAACCTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTTC | | 1095 |

00821" 02482260

Figure 12B.

| | | | | | | |
|-----------|------------|------------|------------|------------|------------|-----|
| human | MRLGSP---- | ----- | -----G | L-LF-LLFSS | LRADTQEKEV | 25 |
| mouse | MQLKCPCFVS | LGTRQPVWKK | LHVSSGFFSG | LGLFLLLLSS | LCAASAETEV | 50 |
| Consensus | M.L..P.... | |G | L.LF.LL.SS | L.A...E.EV | 50 |
| human | RAMVGSDEL | SCACPEGSRF | DLNDVYVYQ | TSESKTVVTY | HIPQNSSLEN | 75 |
| mouse | GAMVGSNVVL | SCIDPHRRHF | NLSGLYVYQ | IENPEVSVTY | YLPYKSPGIN | 100 |
| Consensus | .AMVGS.V.L | SC..P....F | .L...YVYQ |VTY | ..P..S...N | 100 |
| human | VDSRYRNRAL | MSPAGMLRGD | FSLRLFNVTP | QDEQKFHCLV | LSQ-SLGFQE | 124 |
| mouse | VDSSYKNRGH | LSLDSMKQGN | FSLYLKNVTP | QDTQEFTCRV | FMNTATELVK | 150 |
| Consensus | VDS.Y.NR.. | .S...M..G. | FSL.L.NVTP | QD.Q.F.C.V | | 150 |
| human | VLSVEVTLHV | AANFSVPVVS | APHSPSQ-DE | LTFTCTSING | YPRPNVYWIN | 173 |
| mouse | ILEEVVRLRV | AANFSTPVIS | TSDSSNPGQE | RTYTCMSKNG | YPEPNLYWIN | 200 |
| Consensus | .L...V.L.V | AANFS.PV.S | ...S.....E | .T.TC.S.NG | YP.PN.YWIN | 200 |
| human | KTDNSLLDQA | LQNDTVFLNM | RGLYDVVSVL | RIARTPSVNI | GCCIENVLLQ | 223 |
| mouse | TTDNSLIDTA | LQNNTVYLNK | LGLYDVISTL | RLPWTSRGDV | LCCVENVALH | 250 |
| Consensus | .TDNSL.D.A | LQN.TV.LN. | .GLYDV.S.L | R...T..... | .CC.ENV.L. | 250 |
| human | QNLTVGSQTG | NDIGERDKIT | ENPVSTGEKN | AATWSILAVL | CLLVVVAVAI | 273 |
| mouse | QNITSISQAE | SFTGNNTKNP | QETHNNELKV | LV--PVLAVL | AAAAFVSFII | 298 |
| Consensus | QN.T..SQ.. | ...G...K.. |K. |LAVL |V...I | 300 |
| human | GWVCRDRCLQ | HSYAGAWAVS | PETELTGHV | | | 302 |
| mouse | YR--RTR-PH | RSYTGPKTVQ | LE--LTDHA | | | 322 |
| Consensus |R.R... | .SY.G...V. | .E..LT.H. | | | 329 |

00821" 0248360

Figure 13A

| | |
|---|------|
| AACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCTAATACGA | -111 |
| CTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTC | -56 |
| GACCCACGCGTCCGTGAACACTGAACGCGAGGACTGTTAACTGTTTCTGGCAAAC | -1 |
| ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC TTC TGC TTG CGC ATT 45 | |
| M K S G L W Y F F L F C L R I | |
| 5 10 15 | |
| AAA GTT TTA ACA GGA GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG 90 | |
| K V L T *G *E I N G S A N Y E M | |
| 20 25 30 | |
| TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT TTA TGC AAA TAT CCT 135 | |
| F I F H N G G V Q I L C K Y P | |
| 35 40 45 | |
| GAC ATT GTC CAG CAA TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA 180 | |
| D I V Q Q F K M Q L L K G G Q | |
| 50 55 60 | |
| ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA AGT GGA AAC ACA GTG 225 | |
| I L C D L T K T K G S G N T V | |
| 65 70 75 | |
| TCC ATT AAG AGT CTG AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC 270 | |
| S I K S L K F C H S Q L S N N | |
| 80 85 90 | |
| AGT GTC TCT TTT TTT CTA TAC AAC TTG GAC CAT TCT CAT GCC AAC 315 | |
| S V S F F L Y N L D H S H A N | |
| 95 100 105 | |
| TAT TAC TTC TGC AAC CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA 360 | |
| Y Y F C N L S I F D P P P F K | |
| 110 115 120 | |
| GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT TAT GAA TCA CAA CTT 405 | |
| V T L T G G Y L H I Y E S Q L | |
| 125 130 135 | |
| TGT TGC CAG CTG AAG TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT 450 | |
| C C Q L K F W L P I G C A A F | |
| 140 145 150 | |
| GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT ATT TGT TGG CTT ACA 495 | |
| V V V C I L G C I L I C W L T | |
| 155 160 165 | |
| AAA AAG AAG TAT TCA TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC 540 | |
| K K K Y S S S V H D P N G E Y | |
| 170 175 180 | |
| ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA AAA TCT AGA CTC ACA 585 | |
| M F M R A V N T A K K S R L T | |
| 185 190 195 | |
| GAT GTG ACC CTA TAA 600 | |
| D V T L STOP | |
| 199 | |
| TATGGAAGTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCTCAACTTGA 655 | |
| AGTGCAAGATTCTCTTATTTCCGGGACCACGGAGAGTCTGACTTAACTACATACA 710 | |

09723420-112300

TCTTCTGCTGGTGTGTTTTGTTCAATCTGGAAGAATGACTGTATCAGTCAATGGGGA
TTTTAACAGACTGCCTTGGTACTGCCGAGTCCTCTCAAAACAAACACCCCTCTTGC
AACCAGCTTTGGAGAAAGCCCAGCTCCTGTGTGCTCACTGGGAGTGGAATCCCTG
TCTCCACATCTGCTCCTAGCAGTGCATCAGCCAGTAAACAAACACATTTACAAG
AAAAATGTTTTAAAGATGCCAGGGGTACTGAATCTGCAAAGCAAATGAGCAGCCA
AGGACCAGCATCTGTCCGCATTTCACTATCATACTACCTCTTTCTGTAGGGA
TGAGAATTCCTCTTTAATCAGTCAAGGGAGATGCTTCAAAGCTGGAGCTATTTT
ATTTCTGAGATGTTGATGTGAAGTGTACATTAGTACATACTCAGTACTCTCCTTC
AATTGCTGAACCCCAGTTGACCATTTTACCAAGACTTTAGATGCTTTCTTGTGCC

765
820
875
930
985
1040
1095
1150
1205

0082T" 0248260

Figure 13B

| | | |
|-------|---|-----|
| hCRP1 | MKSGLWYFFLFCLRIKVL TGEINGSANYEMFI FHNGGVQILCKYPDIVQQ | 50 |
| mCRP1 | MKPYFCRVFVFCFLIRL L TGEINGSADHRMFSFHNGGVQISCKYPETVQQ | 50 |
| hCRP1 | FKMQLLKGGQILCDLT KTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNLD | 100 |
| mCRP1 | LKMRLFREREVLCELT KTKGSGNAVSIKNPMLCLYHLSNNSVSFFLNND | 100 |
| hCRP1 | HSHANYFNCNLSIFDPPP FKV.TLTGGYLHIYESQLCCQLKFWLPVIGCAA | 149 |
| mCRP1 | SSQGSYYFCSLSIFDPPP FQERNLSSGGYLHIYESQLCCQLKLWLPVIGCAA | 150 |
| hCRP1 | FVVVCILGCILICWLTK KKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL | 199 |
| mCRP1 | FVVVLLFGCILLIWF SKKKYGSSSVHDPNSEYMFMAAVNTNKSRLAGVTS | 200 |

09728420 112800

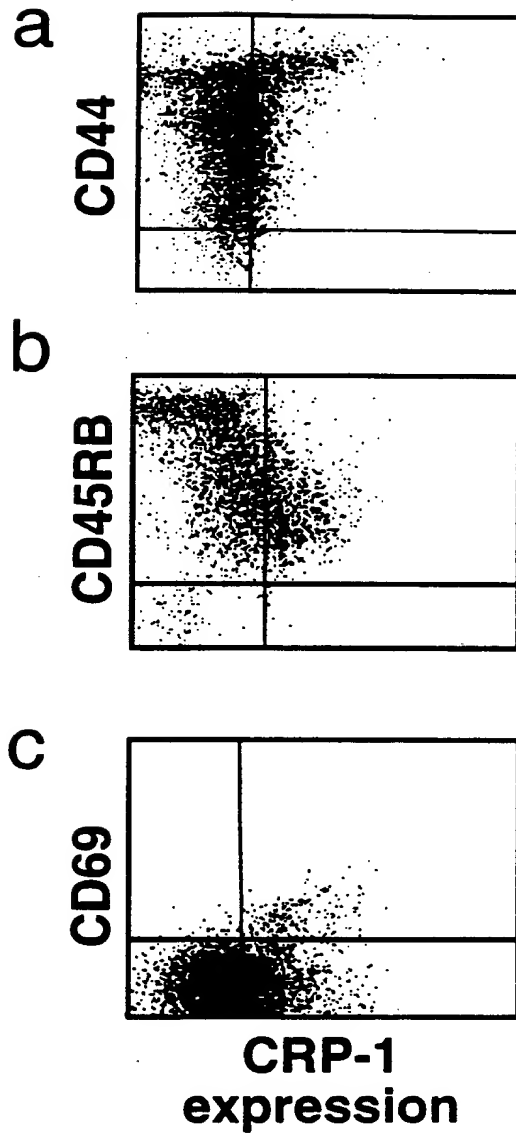


Figure 14

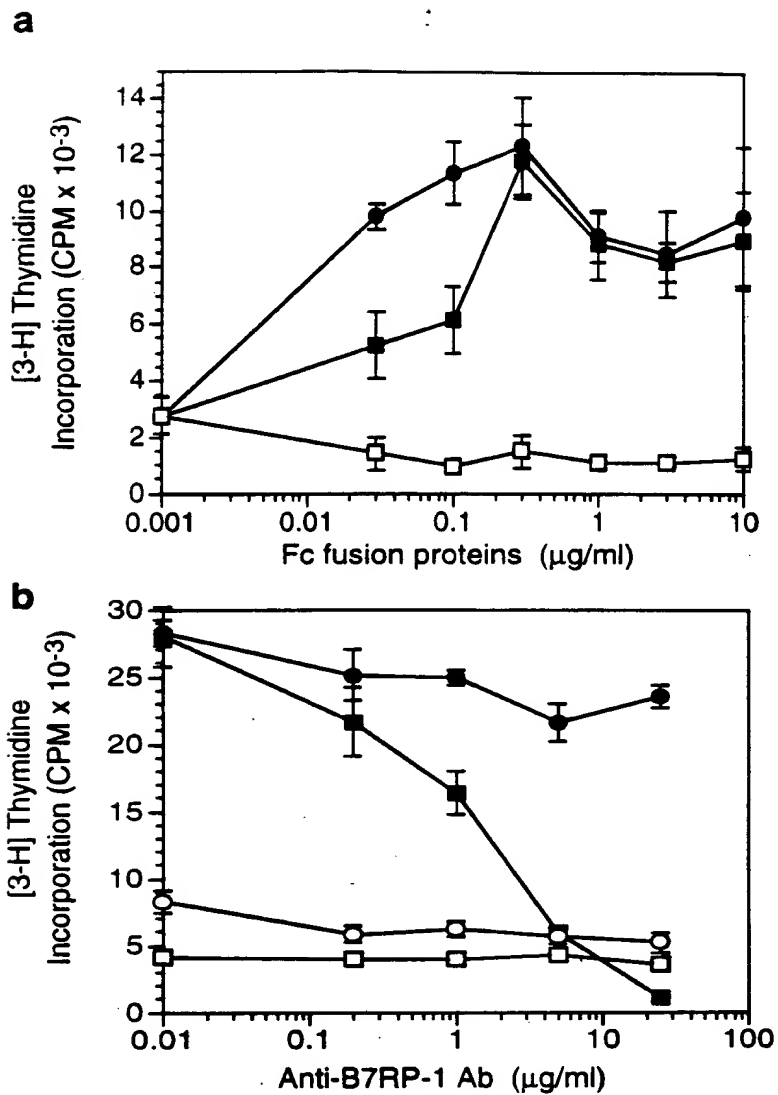
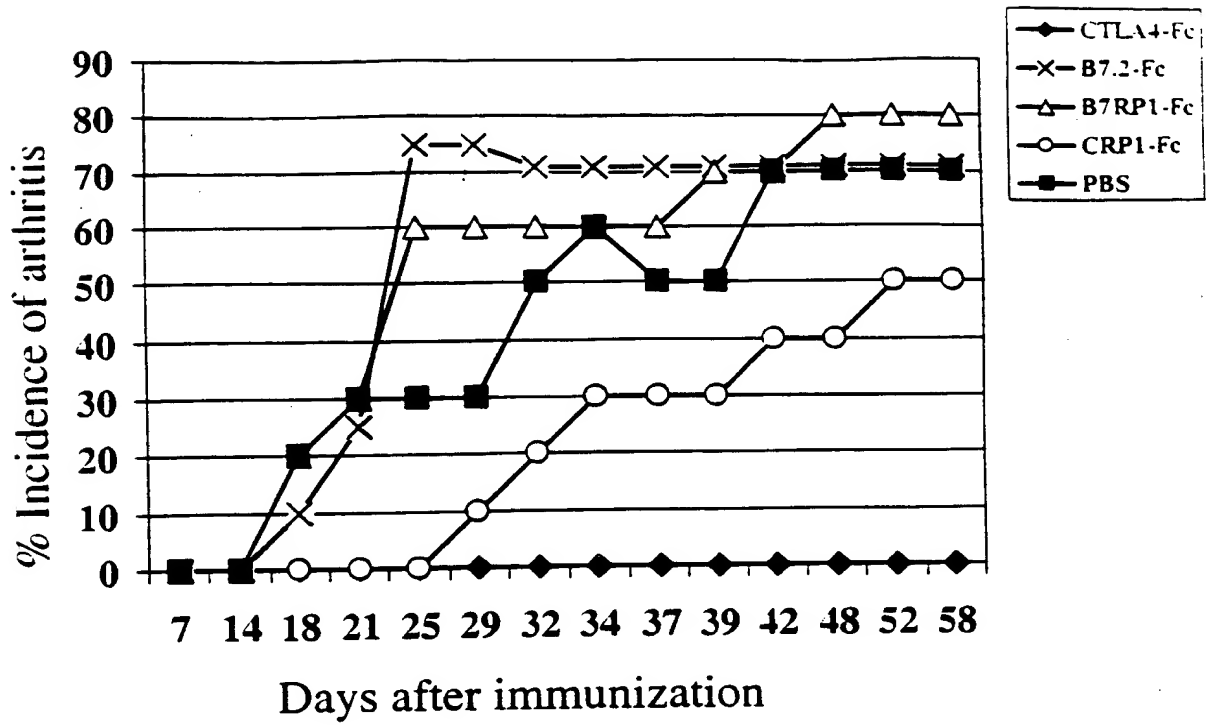


Figure 15

A.



B.

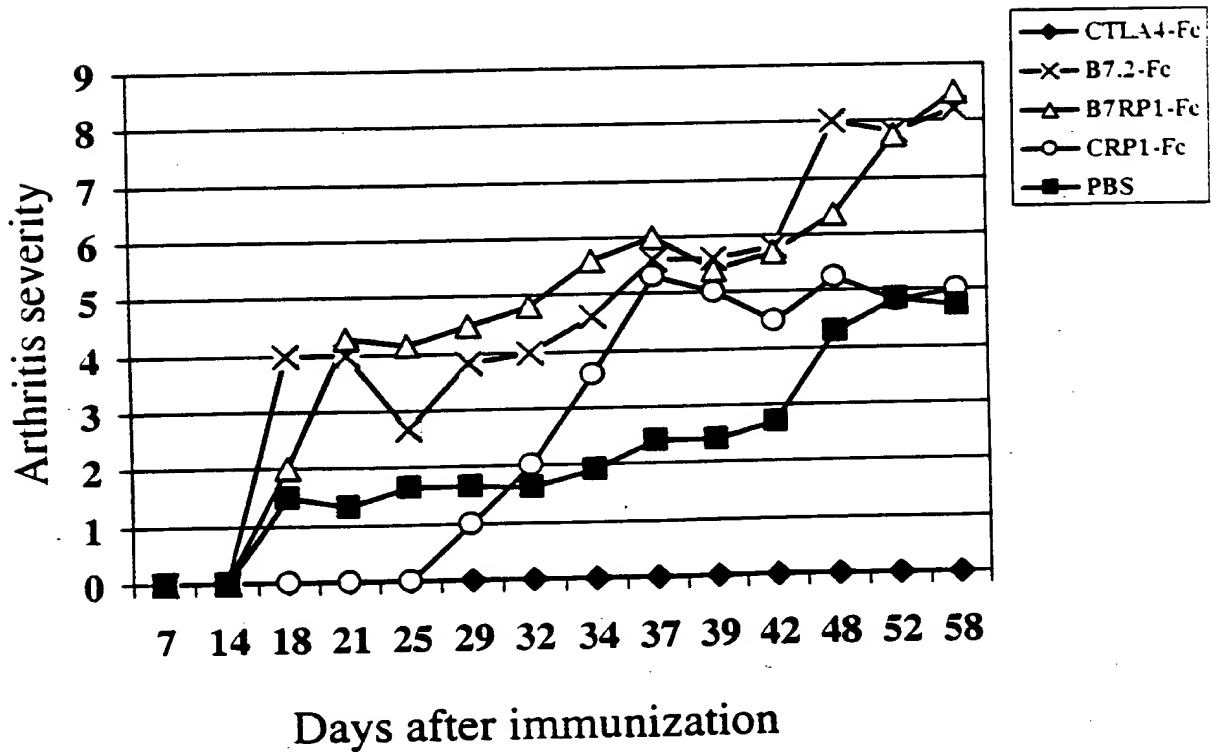
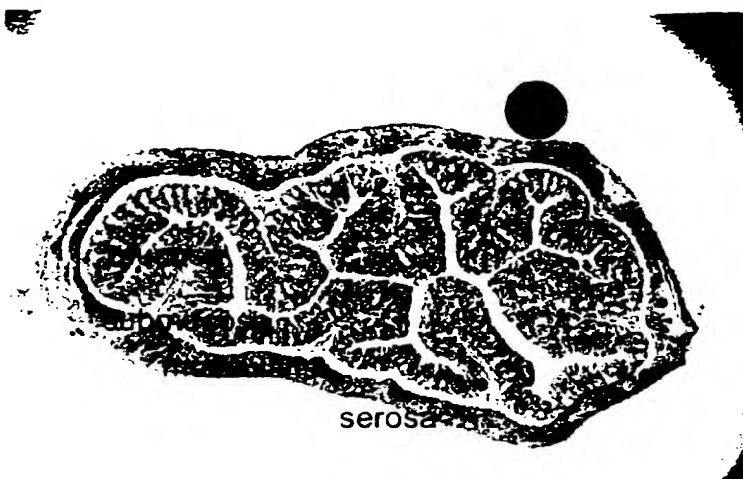


Figure 16



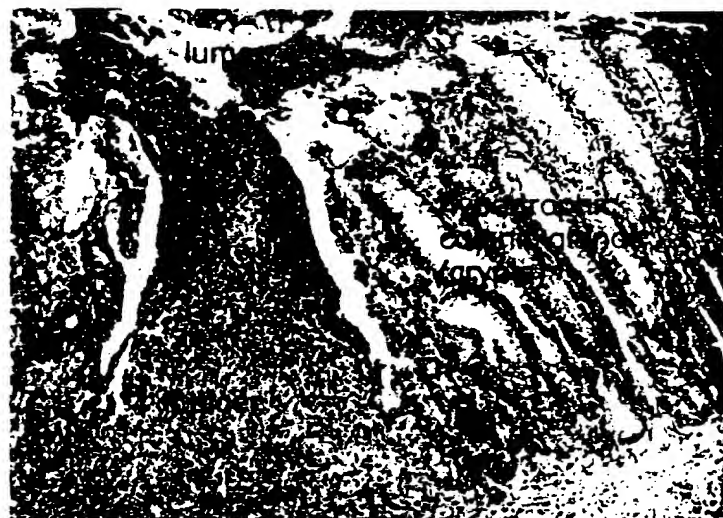
A. Control mouse#53F: Prox. colon 40X



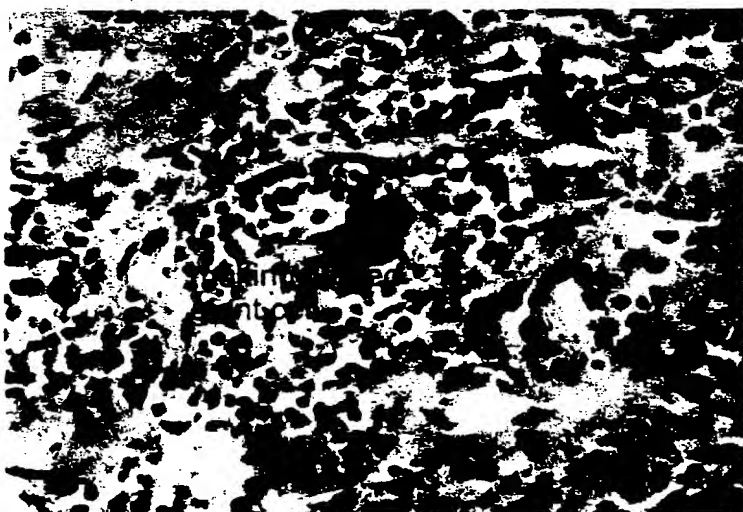
B. Mouse#111F: Prox. colon 40X



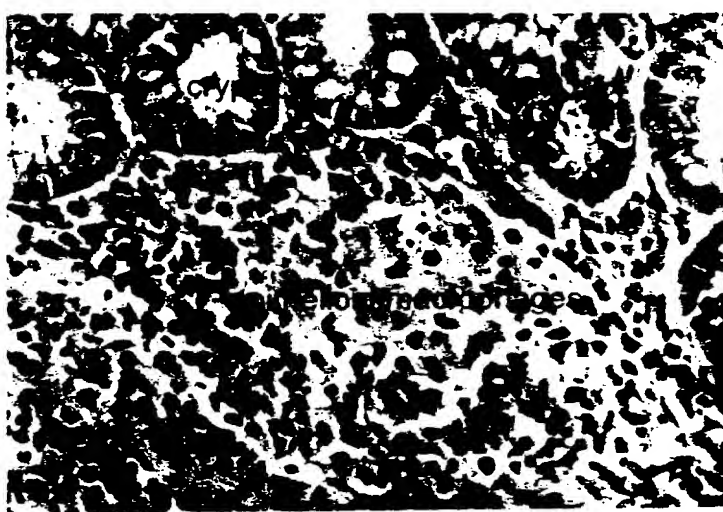
C. Mouse#111F: Prox. colon 20X



D. Mouse#111F: closeup of mucosa 100X

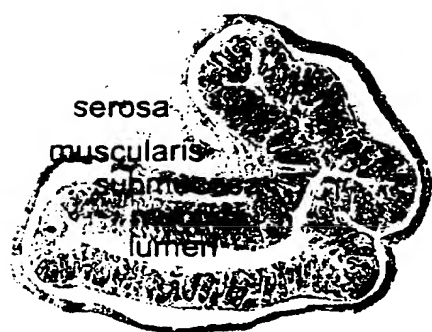


E. Mouse#112F: Giant cell, submucosa

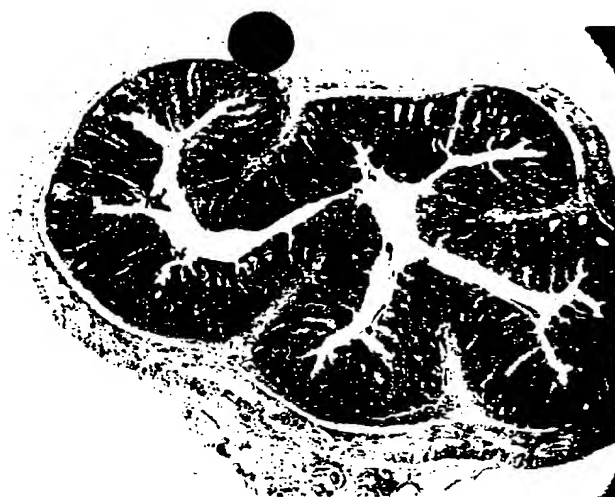


F. Mouse#112F: epithelioid macrophages

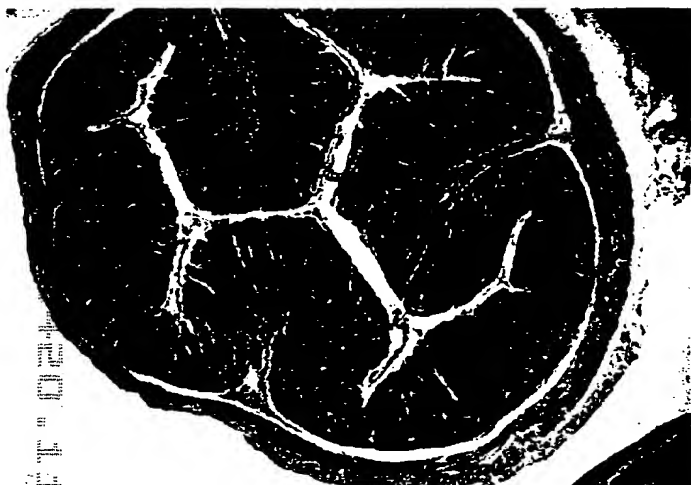
Figure 17



A. Control mouse#53F:Distal colon, 40X



B. mouse#111F:Distal colitis, 40X



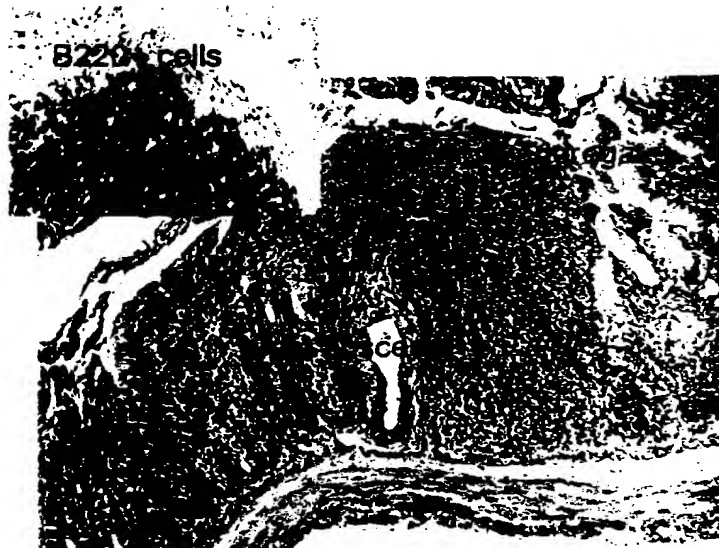
C. mouse#55M:Distal colitis, 40X



D. mouse#112F:Distal colon, 40X



E. mouse#112:CD3+ T-cells, 40X

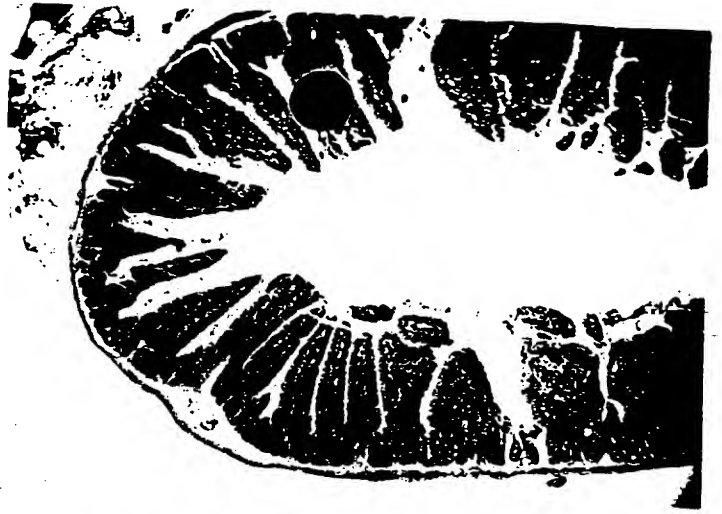


F. mouse#112:closeup, 100X

Figure 18



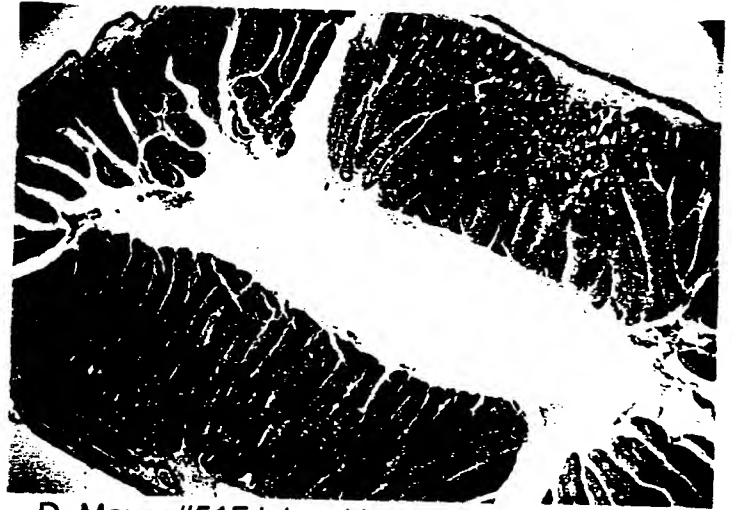
A. Control mouse#53F:duodenum, 40X



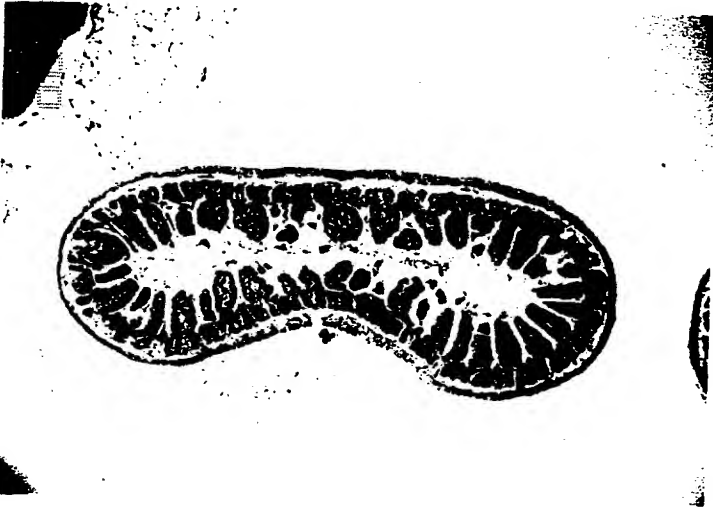
B. Mouse#51F:duodenum, 40X



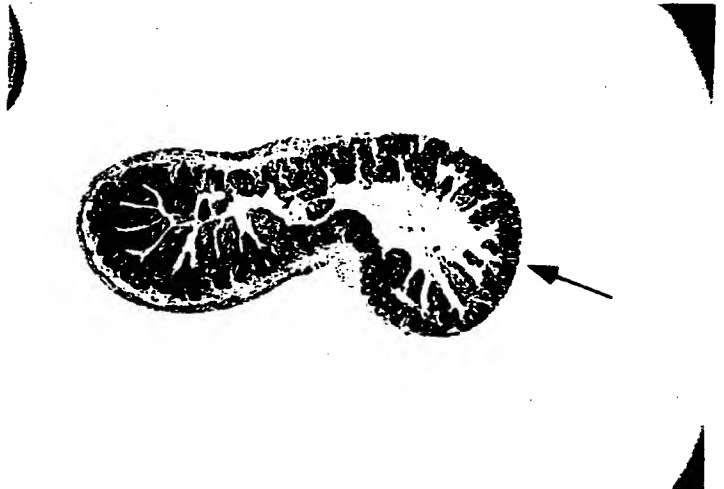
C. Control mouse#53F:jejunum, 40X



D. Mouse#51F:jejunal hyperplasia, 40X



E. Control mouse#53F:ileum, 40X



F. Mouse#231M:ileal atrophy, 40X

Figure 19

Figure 20

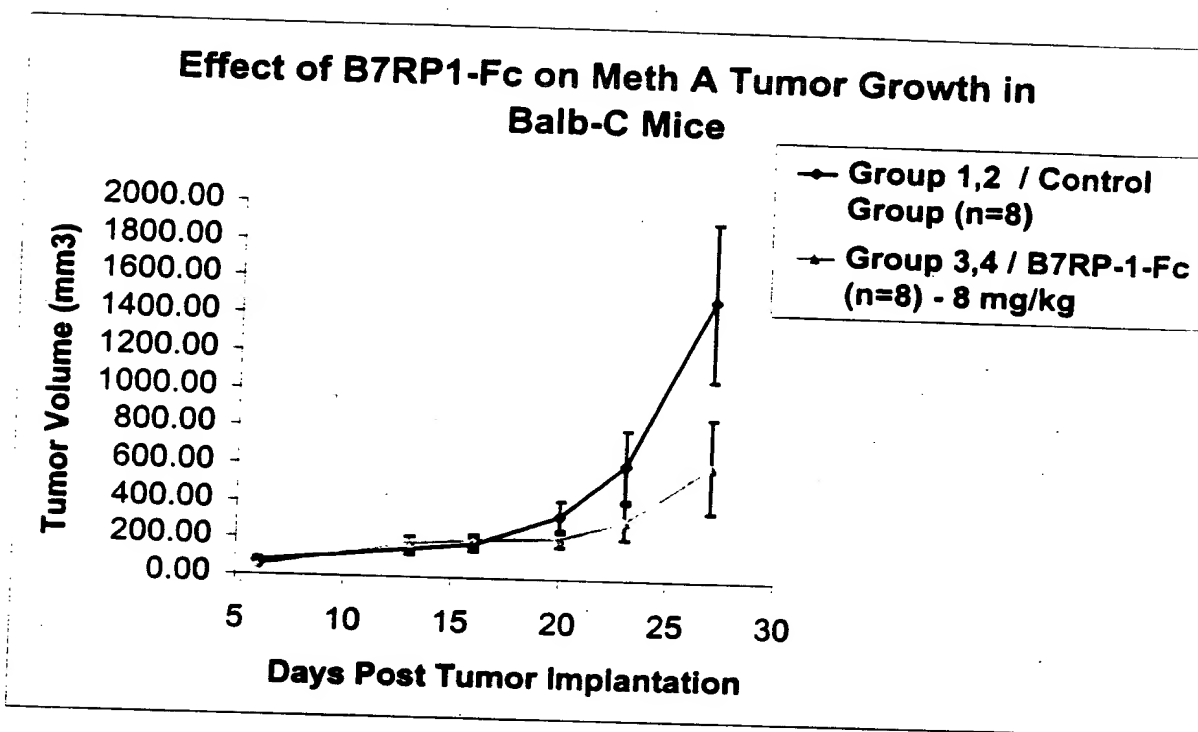


Figure 21A/B.

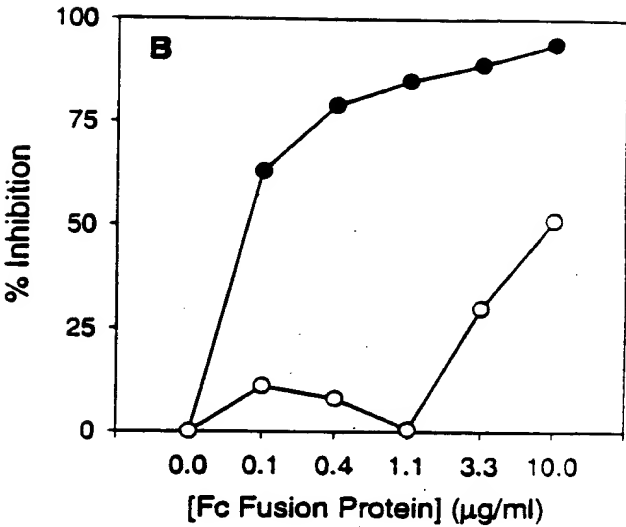
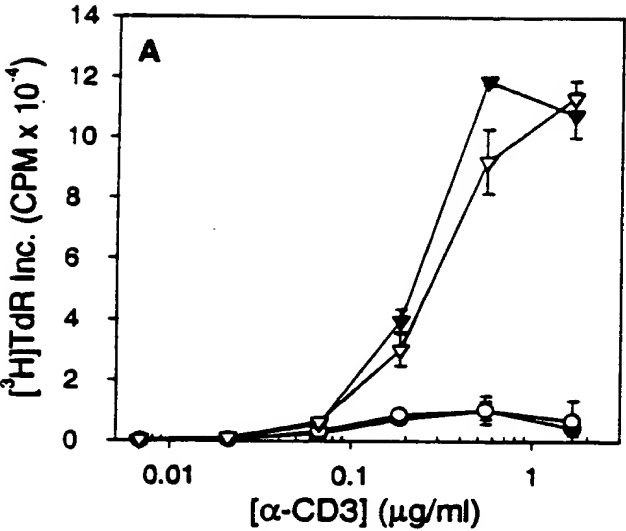


Figure 21C.

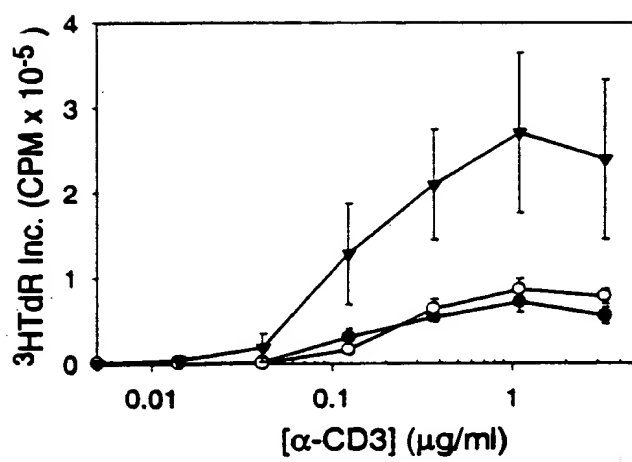
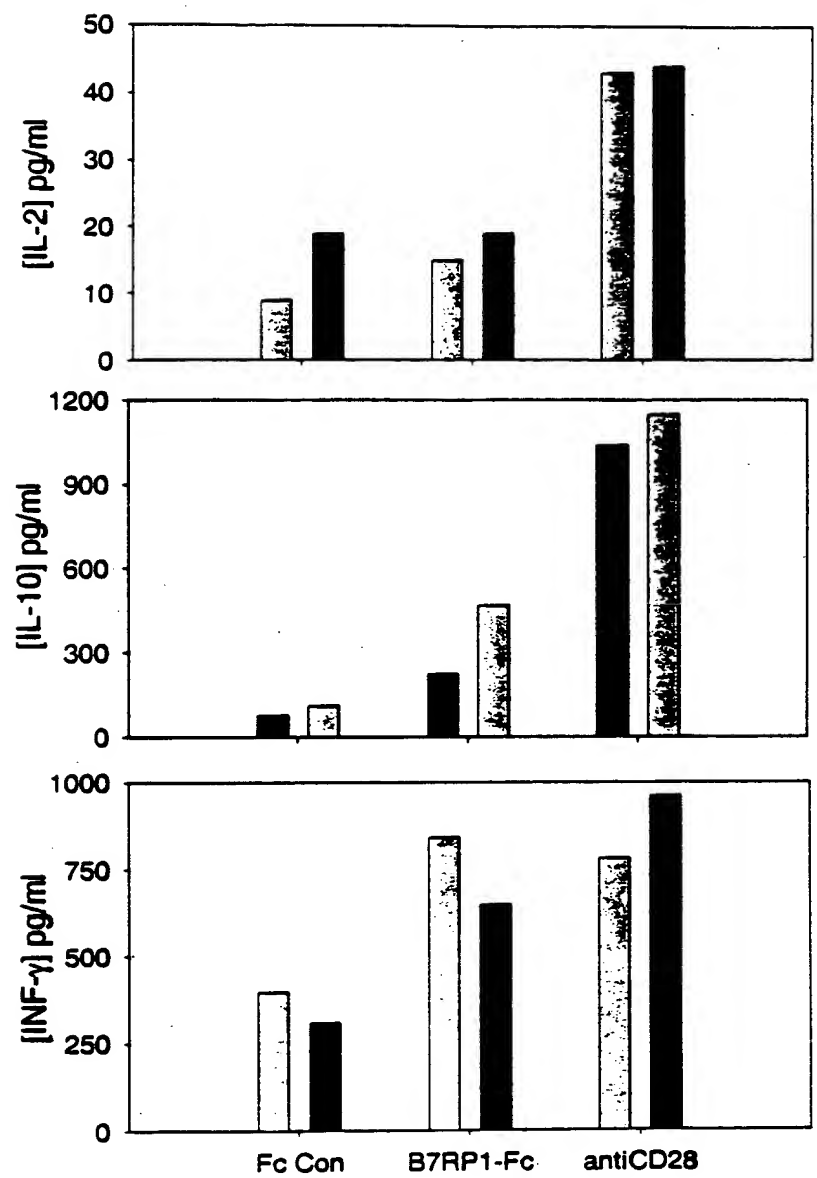


Figure 21D



008217 02482260

Figure 23

